

GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15	CAATGAGTCCGAGATCTTCA 1 GACCTGGAGAGGAGATATG AGGGACAATTG	TGAGTCCGAG 16 ATCTTCAGAC CTGG	GA GAG-- AGA T CAAT GTCC ATCTTC CC G GTTA CAGG TAGAGG GG G A- GAGTA A-- A
GAM16	CATATGTATGTTTCAGGGAA 2 AGCTAGGGGATGGTTTATA GACATCACTATG	TTTTATAGAC 17 ATCACTATG	- T CAGGG GG CATA TG ATGTTT AAAGCTA G GTAT AC TACAGA TTTTGGT / C - TA--- AG
GAM17	CCACTCTATTTTGTGCATCA 3 GATGCTAAAGCATATGATAC AGAGGTACATAATGTTTGG	TATGATACAG 18 AGGTACATAA TGTT	CTC T ----- G T CCA TATT TGTC ATCA ATGC A GGT GTAA ACATG TAGT TACG A TT- T GAGACA A A
GAM18	CCATAATGATGCAGAGAGGC 4 AATTTTAGGAACCAAGAAA GATTGTTAAGTGTTCATTT GTGG	TTAAGTGTTT 19 CAATTGTGG	- T GAGA AGGAA CCATAAT GA GCA GGCAATTTT C GGTGTTA CT TGT TTGTTAGAA C A T GAA- AGAAA
GAM19	CCATTGACAGAGAAAAAAT 5 AAAAGCATTAGTAGAAATTT GTACAGAGATGG	TGACAGAAGA 20 AAAAATAAAA GCAT	--- - AGAAAAA AA CCAT TG ACAGA TAA G GGTA AC TGTTT ATT / GAG A AAAGATG- AC
GAM20	CCTCTATTGTGTGCATCAA 6 GGATAGAGATAAAAGACACC AAGGAAGCTTTAGACACAGAT AGAGG	TATTGTGTGC 21 ATCAAGGAT AGAG	G ----- A AAA ATAGAGA T CCTCTATT TGT GC TC GG GGAGATAG ACA CG AG CC A A GATTT A GAA ACAGAAA
GAM21	GAATAGTTTTTGTGTACTT 7 TCTATAGTGAATAGAGTTAG GCAGGGATATTC	TAGTTTTTGC 22 TGTACTTTCT ATAG	G GTACT AG GAATA TTTTGTCT TTCTAT T CTTAT AGGGACGG GAGATA / - ATT-- AG

GAM22	GCCACATACCTAGAAGAATA 8 AGACAGGGCTTGGAAAAGGAT TTGCTATAAGATGGGTGGC AAGTGGT	TAAGATGGGT 23 GGCAAGTGGT	A--- GAAGAATA A - G GCCAC TACCTA AG CAGG CTT G TGGTG GTGGGT TC GTTTT GGA A AACG AGAATA-- - A A
GAM23	GGAGACAGCGACGAAGAGCT 9 CATCAGAAACAGTCAGACTCA TCAAGCTTCTCT	CAGACTCATC 24 AAGCTTCTCT	C GAC A - C CAG GGAGA AGC GA GAG CT AT A TCTCT TCG CT CTC GA TG / - AA- A A C ACA
GAM24	GGTCCAAAATGCGAACCCAG 10 ATTGTAAGACTATTTTAAAA GCATTGGGACC	TCCAAAATGC 25 GAACCCAGAT TGTA	AA GAACCC T TA GGTCC AATGC AGAT G A CCAGG TTACG TTTA C / G- AAAAT- T AG
GAM25	GTACTGGGTCTCTGTGTTA 11 GACCAGATCTGAGCCTGGGA GCTCTCTGGCTAACTAGGGA ACCCACTGC	TCTCTGGTTA 26 GACCAGATCT GAGC	C C A TCT CT GTA TGGGT TCTCTGGTTAG CCAGA GAGC G CGT ACCCA AGGGATCAATC GGTCT CTCG G C - - - - - AG
GAM26	TAATTGGAAGAAAATCTGTTG 12 ACTCAGATTGGTTGCACCTTT AAATTTTCCCATTA	TTGTTGTCAC 27 TTTAAATTTT CCCA	T ----- TT TAAT GGAAGA AATCTG G ATTA CCTTTT TTAGAC A C AAATTTTCACGTTGG TC
GAM27	TCTTTTGGCAACGACCCCTCG 13 TCACAAATAAAGATAGGGGGG CAACTAAAGG	TGGCAACGAC 28 CCCTCGTCAC AATA	CAACGA CG ACA TCTTTGG CCCCT TC A GGAAATC GGGGG AG T AACG-- AT AAA
GAM28	TTACCCATATAGTGCAGAAACA 14 TCCAGGGGCAAAATGGTACAT CAGGCCATATCACCTAGAAC TTTAAATGCATGGGTAA	TATAGTGCAG 29 AACATCCAGG GGCA	TATA GAACA--- C GGCAA ACA TTACCC GTGCA TC AGG ATGGT T AATGGG TACGT AG TCC TACCG / ----- AAATTTCA A ACTA- GAC

GAM29

TTCATTGCCCAAGTTTGTTC 15
ATAACAAAAGCCTTAGGCAT
CTCCTATGGCAGGAA

AGCCTTAGGC 30
ATCTCCTATG
GCAG

A AG----- T
TTC TTGCCA TTTGTT C
||| |||||
AAG GACGGT AAACA A
- ATCCTCTACGGATTCCGA T

GENE	TARGET	UTR SEQUENCE	SEQID	BINDING-SITE
GAM15	PRIM2A	3' CAGGCAGATCTCAGACTC	50	<p>=====</p> <p>C TCAGA</p> <p>GAGTC GAGATCT CCTG</p> <p> </p> <p>CTCAG CTCTAGA GGAC</p> <p>A C</p> <p>A CCG A</p> <p>TG GT AG TCCTCAGACCTGG</p> <p> </p> <p>AC CG TC AGAAGTCTGGACC</p> <p>C TTG A</p>
GAM15	RAP1B	3' CCAGGTCTGAAGAACTGTTGCC	142	<p>CA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p>
GAM15	RET	3' CCAGGTCTTAAACAGCTGACCCA	173	<p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p>
GAM15	RET	3' CCAGGTCTTAAACAGCTGACCCA	174	<p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p>
GAM15	RET	3' CCAGGTCTTAAACAGCTGACCCA	179	<p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p>
GAM15	RET	3' CCAGGTCTTAAACAGCTGACCCA	37	<p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p> <p>A CG ATCTTC</p> <p>TG GTC AG AGACCTGG</p> <p> </p> <p>AC CAG TC TCTGGACC</p> <p>C GACAAA</p>
GAM15	AMOTL1	3' CTGATAAAGATTTTCAGACTCA	304	<p>C</p> <p>TGAGTC GAGATCT TCAG</p> <p> </p> <p>ACTCAG CTTTAGA AGTC</p> <p>A AAT</p> <p>G A C AC</p> <p>TGAGTCC AG TCCT AG CTGG</p> <p> </p> <p>ACTCAG TC GGGA TC GACC</p> <p>CA</p>
GAM15	DGKZ	3' CCAGACCTAGGGCTGGACTCA	70	<p>A</p> <p>TGAGTCC AG TCCT AG CTGG</p> <p> </p> <p>ACTCAG TC GGGA TC GACC</p> <p>CA</p>
GAM15	DKFZP586G1122	3' CAGGTCTAGCCGGGCCCA	265	<p>A</p> <p>TGAGTCC AG TCCT AG CTGG</p> <p> </p> <p>ACTCAG TC GGGA TC GACC</p> <p>CA</p>
GAM15	FLJ22127	3' CCAGGCCTGAATGGATGGACTC	192	<p>A</p> <p>TGAGTCC ATCT TCAG CCTGG</p> <p> </p> <p>AC CCGGC GA TCTGGAC</p> <p>C</p> <p>GAG</p>

GAM15	LOC126248	3'	CAGCCCTGGCTGACTC	308	<p>ACTCAGG TAGG AGTC GGACC</p> <p>G ATCT AC TA C</p> <p>GAGTCC AG TCAG CT G</p> <p> </p> <p>CTCAGG TC GGTC GA C</p>
GAM15	LOC146640	5'	CCAGGTGACCTACCCGGACTCA	323	<p>- AGATCT AG CC A</p> <p>TGAGTCCG TC ACCTGG</p> <p> </p> <p>ACTCAGGC AG TGGACC</p> <p>CCATCC -</p>
GAM15	LOC153416	3'	CCAGGTCTGAAGAACTGTTGCC	263	<p>A CCG A</p> <p>TG GT AG TCCTCAGACCTGG</p> <p> </p> <p>AC CG TC AGAAGTCTGGACC</p> <p>C TTG A</p>
GAM15	LOC220790	3'	CCAGGTCTGAAGAACTGTTGCC	378	<p>A CCG A</p> <p>TG GT AG TCCTCAGACCTGG</p> <p> </p> <p>AC CG TC AGAAGTCTGGACC</p> <p>C TTG A</p>
GAM16	PRKG2	3'	CATGGTGGTATCTTAAAA	103	<p>T C</p> <p>TTTTA AGA ATCACTATG</p> <p> </p> <p>AAAAT TCT TGGTGGTAC</p>
GAM16	AFAP	3'	CATAGCAGGGCGTCTGTAAAA	183	<p>- A A A A</p> <p>TTTTATAGAC TC CTATG</p> <p> </p> <p>AAAATGTCTG GG GATAC</p> <p>CG AC</p>
GAM16	C3AR1	3'	CATAGTGAAGTTTATAAGA	76	<p>A A</p> <p>TTTTATAGAC TCACATATG</p> <p> </p> <p>AGAATATTG AGTGATAC</p> <p>AA</p>
GAM16	FLJ22029	3'	CATGAAAAATGTCTATAGAA	203	<p>CAC</p> <p>TTTTATAGACAT TATG</p> <p> </p> <p>AAGATATCTGTA GTAC</p> <p>AAA</p>
GAM16	SEMA5A	3'	CATAGTGACGTCCTGAAGA	72	<p>ATA A</p> <p>TTTT GAC TCACATATG</p> <p> </p> <p>AGAA CTG AGTGATAC</p> <p>GTC C</p>
GAM16	UNC5D	3'	CATAGGATTTCTATAGAA	234	<p>C A</p> <p>TTTTATAGA ATC CTATG</p> <p> </p>

GAM16	LOC129446	3'	CATAGAATGTGTCTATAAA	315	<p>AAGATATCT TAG GATAC</p> <p>T CA_</p> <p>TTTATAGACAT CTATG</p> <p> </p> <p>AAATATCTGTG GATAC</p> <p>TAA</p>
GAM16	LOC153396	3'	CATAGTGGCTGCCCTATAGAA	338	<p>A A_ TCACATAG</p> <p>TTTATAG CA_ TCACATAG</p> <p> </p> <p>AAATATCTGTG GATAC</p> <p>TAA</p>
GAM16	LOC50999	3'	CATAATGGTGTCTTAAAA	145	<p>T C</p> <p>TTTTA AGACATCA TATG</p> <p> </p> <p>AAAT TCTGTGGT ATAC</p> <p>A</p>
GAM17	KIAA0830	3'	AACATTATGCTTACTGCATC	290	<p>A TA</p> <p>GAT CAG AGG CATAATGTT</p> <p> </p> <p>CTA GTC TTC GTATTACAA</p> <p>C A</p>
GAM17	PREI3	3'	AACATTATGCTTACTGTATATATC	275	<p>ATGATA GGTACATAATGTT</p> <p> </p> <p>TACTAT TCAATGATTACAA</p> <p>ATATG</p>
GAM17	SEC15L	3'	ACATATGCCCTCTACTCAT	297	<p>TAC CATA</p> <p>TATGA AGAGGTA ATGT</p> <p> </p> <p>ATACT TCTCCGT TACA</p> <p>CA_ GTA A_</p>
GAM17	LOC152317	3'	AACATCAATGGACTCTGTATCA	352	<p>TGATACAGAG CAT ATGTT</p> <p> </p> <p>ACTATGTC GTA TACAA</p> <p>AG_ AC</p>
GAM18	DSCR1	3'	CATTTTGAATACTTAA	81	<p>TTAAGTGTTC GTG</p> <p> </p> <p>AAATCATAAAGTT TAC</p> <p>T</p>
GAM18	ELMO2	3'	CCAGGAGAAACACTTA	235	<p>AA G</p> <p>TAAGTGTTC TT TGG</p> <p> </p> <p>ATTCACAAAG AG ACC</p> <p>G</p>
GAM18	ELMO2	3'	CCAGGAGAAACACTTA	186	<p>AA G</p> <p>TAAGTGTTC TT TGG</p> <p> </p> <p>ATTCACAAAG AG ACC</p> <p>G</p>

GAM18	PGF5	3'	CCACAGGGAGCAAAACACTTAG	227	ATTCACAAAG AG ACC G CAA__TTGTGG TTAAGTGTTC GATTCACAAA GACACC CGAGG
GAM18	PGF5	3'	CCACAGGGAGCAAAACACTTAG	83	CAA__TTGTGG TTAAGTGTTC GATTCACAAA GACACC CGAGG
GAM18	NEFH	3'	CCACACGTAAACACTTGA	180	CAAT TGTGG TTAAGTGTTC AGTTCACAAA ACACC TGC_
GAM18	NFIB	3'	CCACAAAAAGAAACACTTAA	93	AA TTAAGTGTTC TTGTGG AATTCACAAAG AACACC AA
GAM18	PRKY	3'	CCATAAATGAAACACTTGA	62	A TTAAGTGTTC TTGTGG AGTTCACAAAGT AATACC A
GAM18	RNF18	5'	CCACAAATTGGGTTCTTA	172	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT_
GAM18	SLC1A3	3'	CCACAAATTGAAATTTTAA	77	T_
GAM18	VMD2	3'	CCATTGGAACATTTAA	78	TTAAG GTTTC AATT TTAAGTGTTC GTGG AATTT TAAAGTTAACACC T
GAM18	XRCC3	5'	CCAGGGAGACACTTAA	91	GT_ G AAT_ G TTAAGTGTTC T TGG AATTCACAGAG G ACC G
GAM18	ARHGAP5	3'	CTATATGAAACATTTAA	321	AT TTAAGTGTTC TTGTGG

GAM18	EFA6R	3'	CCATTGCGAAACACTTAA	140	AATTTCACAAAGT ATATC ATT TTTAAGTGTTC GTGG AATTTCACAAAGT TACC GT- T AT TAAGTGTT CA TGTGG ATTCACAA GT ACACC T GTGTTT CAATTGTGG TACAAG GTTAACACC TCT TTAAGTGTTT AT TGG AATTACAAG TG GTC AA GT AA TTAAGTGTTC TTGTGG AGTTCACAAAG AACACC GTC TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT- TTAAGTGTTC TTG TGG AATTTCACAAAG AAC ACC AA T ATT TTAAGTGTTC GTGG AATTTCACAAAGT CACC
GAM18	KIAA0903	3'	CCACATGTAAACACTTA	294	
GAM18	KIAA1244	3'	CCACAATTGTCTGAACAT	295	
GAM18	Rpo1-2	3'	CTGTGGTAAGAACACTTAA	214	
GAM18	LOC115574	3'	CCACAACCTGGAACACTTGA	303	
GAM18	LOC144144	5'	CCACAATTGGGTTCTTA	260	
GAM18	LOC148254	3'	CCATCAAAAGAAACACTTAA	329	
GAM18	LOC157624	5'	CCACTGAAACATTTAA	359	
GAM18	LOC220486	5'	CCACAATTGGGTTCTTA	374	
GAM19	AGL	3'	ATGCTTTTCATTTTTTCACTG	31	TGT TAAG TTCAATTGTGG ATTC GGGTTAACACC TT- AA CAG GAAAAAAT AAAGCAT

Gene	Accession	Position	Sequence	Length
GAM19	AGL	3'	ATGCTTTCAATTTTTTCACTG	43
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	AGL	3'	ATGCTTTCAATTTTTTCACTG	44
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	AGL	3'	ATGCTTTCAATTTTTTCACTG	45
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	AGL	3'	ATGCTTTCAATTTTTTCACTG	46
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	AGL	3'	ATGCTTTCAATTTTTTCACTG	47
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	ALB	5'	GCCTTTCTCTCTCTGCA	40
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	CKN1	3'	TTTTATTCTTTCTTCTTCA	32
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	HHIP	3'	TTTATTATTTTATCCCTGTCA	189
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	IFNA1	3'	GCCTTTCATGAATTCTGTCA	194
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	
GAM19	KCNJ6	5'	TTTTTTTTTTTTTCTTCTGTCCA	60
			A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA A ⁻ C AA ⁻ A CAG GAAAAAAT AAAGCAT GTC CTTTTTTA TTTCGTA	

Gene	Accession	Position	Sequence	Length
GAM19	OTP	3'	GCCTTTATTTTATTTATC	212
GAM19	RHEB2	3'	ATGCTTCTTTTCTCTGTTA	94
GAM19	ANKRD6	3'	ATGCTTTTATTCCTTTTGTTA	137
GAM19	EVI5	3'	TGCAGGTTTTTCTCTTCA	95
GAM19	FLJ00026	3'	ATGCTTTTGCTTTTTTCTTTATG	270
GAM19	GP5	3'	ATGCTCATATCATTTTCTCTT	84
GAM19	KHDRBS3	3'	ATGCTAGTTTTTTTCTCTT	107
GAM19	KIAA0254	3'	TGCTGTGTTCTTCTGTCA	132
GAM19	KIAA1165	3'	ATGCTTTATAACCTCTCTGT	281
GAM19	KIAA1240	3'	GTGGCCATTTTTTCTTCTGTCA	277

GAM19	NYD-SP15	3'	ATGCCATTTTTTTTCTTCTGT	209	ACTGTCCTTCTTTTTTA TG CCGG TAAAA ACAGAAGAAAAA GCAT TGCTCTCTTTTT CGTA TTAC_
GAM19	PEL11	5'	GCTTTACTCTTTTCTTCTGTC	175	GACAGAAGAAA AAAGC CTGCTCTCTTT TTTCC CTCA_
GAM19	PRO0159	5'	TTATTTTTCCTTGTC	125	AA TGACAG GAAAAAATAA ACTGTT CTTTTTATT
GAM19	RACGAP1	3'	ATGTGAGCTTTTCTTCTGTTA	121	C_ ATAAAA TGACAGAAGAAAA GCAT ATTGCTCTCTTTT TGTA
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	118	A TGACAGAAGAAAA ATAA ATTGCTCTCTTT TATT
GAM19	SDFR1	3'	TTATCTTTTCTTCTGTTA	151	C A TGACAGAAGAAAA ATAA ATTGCTCTCTTT TATT
GAM19	SS18L1	3'	TTATCTATCTTCTGTC	272	AAA TGACAGAAGA AATAA ACTGCTCTCT TATT
GAM19	SV2B	3'	ATGTTTACTCTCTCTGTC	136	ATC AAAAAATAA TGACAGAAG AAGCAT ACTGCTCTC TTTGTA
GAM19	LOC130589	3'	TGCTTTTATTCTCTCTCTTC	244	CA A AA TGA GA GA AATAAAGCA ACT CT CT TTTATTTTCGT
GAM19	LOC200107	3'	ATGCTTTTACTTTTCTTTT	364	TC C CC A AGAAGAAAA TAAAGCAT

GAM19	LOC203340	3'	TGCTTTTATTTTCCTTC	368	TTTTCTTTTT ATTTTCGTA C AA GAAG AAAATAAAAGCA CTTC TTTTATTTTCGT C- ATAAAA TGACAGAGAAAAA GCA ACTGTCCTTTTTTTT CGT C C AAATAAA TGA AGAAGAA AGCAT ACT TCCTCTTT TCGTA A A A AGA GA AAAATAAAAGC TCT CT TTTTATTTTCG C C TGACAGAGAA AAATAAAAG -ACTGTCCTTTT TTTATTTT C AAAA GAAG AATAAAAGCAT CTTC TTTTATTTTCGTA CATG A AAA ACAGAGAAAA AT GCA TGTCTTCTTTT TA CGT C G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G G AAG TT TGTGCATCA GATAG AA ACACGTAGT CTATC G TATTGTGTGCAT AGGA AGAG
GAM19	LOC221271	3'	TGCCCTTTTTTTTCTGTCA	380	
GAM19	LOC254778	3'	ATGCTTTTCTTCTATCA	400	
GAM19	LOC51312	5'	GCCTTTTATTTTCTCCTCT	164	
GAM19	LOC91286	5'	TTTTTATTTCTTTTCTGTCA	273	
GAM19	LOC92223	3'	ATGCTTTTATTTGTACCTTC	286	
GAM19	LOC92482	5'	TGCATCTTTTCTTCTGT	288	
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	
GAM20	ATRN	3'	CTATCTGATGCACAGAA	248	
GAM20	DKFZP564O0463	3'	CTTTTCTTTAATGCATACATA	127	CAA T TATTGTGTGCAT AGGA AGAG

GAM20	DKFZP56400463	3'	CTTTTCTTAAATGCATACAATA	127	ATAACATACGTA	TTCT TTTC	A_ T	CAA T	TATTGTGTGCAT	AGGA AGAG			ATAACATACGTA	TTCT TTTC
GAM20	FLJ13102	3'	CTCTACCCCTCTCCCAACACACA	202	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	FLJ13102	3'	CTCTACCCCTCTCCCAACACACA	202	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	HSPC014	3'	CTGTAATTTGATGTACACAA	144	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	HSPC014	3'	CTGTAATTTGATGTACACAA	144	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	KIAA0040	3'	TCTATCCCCTTGTACATA	129	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	KIAA0040	3'	TCTATCCCCTTGTACATA	129	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	KIAA0040	3'	CCACTTGATGCACAAATA	134	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	KIAA0040	3'	CCACTTGATGCACAAATA	134	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG
GAM20	KIAA1908	5'	CTCTCGGGCGATGCACACAA	302	TATTGTGTG	CATCAA_ A	AGG TAGAG			ATGACACAC	TCC ATCTC	CACCCTC C	TATTGTGTG	AGG TAGAG

GAM20	KIAA1908	5'	CTCTCGGGCGGATGCACAAA	302	AACACACGTAG TCTC CGGGC AAAGGAT TTGTGTGCATC AGAG AACACACGTAG TCTC CGGGC TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG G G TTGT TGCATCAAAG ATAG AACA ACGTAGTTTT TGTC A G G TTGT TGCATCAAAG ATAG AACA ACGTAGTTTT TGTC A GGA TATTGTGTGCATCAA TAGAG ATAACATACGTAGTTT GTTTC G GGA TATTGTGTGCATCAA TAGAG ATAACATACGTAGTTT GTTTC G AAAG GATAG TGTTGTGCATC ACACACGTAG CTATC GTGTA AAAG GATAG TGTTGTGCATC ACACACGTAG CTATC GTGTA T G CAAA TATTG GT CAT GGATAGAG
GAM20	MGC22014	3'	CTCTATCCCTTGTTATATCACAAT	269	
GAM20	MGC22014	3'	CTCTATCCCTTGTTATATCACAAT	269	
GAM20	TNRC9	3'	CTGTATTTTGTATGCAACAA	293	
GAM20	TNRC9	3'	CTGTATTTTGTATGCAACAA	293	
GAM20	LOC116123	3'	CTTTGGTTTGTATGTCATAATA	243	
GAM20	LOC116123	3'	CTTTGGTTTGTATGTCATAATA	243	
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	
GAM20	LOC149721	3'	CTATCATGTGGATGCACACA	334	
GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA	354	

GAM20	LOC153338	5'	CTCTATCCCTCTGTGGCCAATA	354	ATAAC CG GTG CCTATCTC TCTC T G CAAA TATTG GT CAT GGATAGAG ATAAC CG GTG CCTATCTC TCTC
GAM20	LOC220766	3'	CCACTTGATGCACAAATA	375	G - - A_ TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA G A_ TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	LOC220766	3'	CCACTTGATGCACAAATA	375	G A_ TATT TGTGCATCAA GG ATAA ACACGTAGTT CC CA
GAM20	LOC253351	5'	CTGGCACCTGATGCACACAA	402	- AAGGA TTGTGTGCATCA TAG AACACACGTAGT GTC CCACG
GAM20	LOC253351	5'	CTGGCACCTGATGCACACAA	402	AAGGA TTGTGTGCATCA TAG AACACACGTAGT GTC CCACG
GAM20	LOC257484	3'	CTCTATCCCTTGTTATATACAAAT	366	TGTCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG TGCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG
GAM20	LOC257484	3'	CTCTATCCCTTGTTATATACAAAT	366	TGTCATCA TATTGTG AAGGATAGAG ATAACAC TTCCTATCTC TATATG
GAM21	KIAA1843	3'	ATAGAAAAGTAGCCAAAAA	267	CTG TTTTTG TACTTTCTAT AAAAAC ATGAAAAGATA CG
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA	117	T TAG TTTTGCTGTACTTT ATC AAAACGACATGAAA C
GAM21	SDFR1	3'	AAAGTACAGCAAAACCTA	150	T TAG TTTTGCTGTACTTT

GAM21	LOC132617	3'	CTACAGACCATAGCAAAAAC	314	ATC AAAACGACATGAAA C ACTT A GTTTTGTGCTGT TCT TAG CAAAAACGATA AGA ATC CC C TGTACT GTTTTGTG TTCTATAG CAAAAACG AAGATATC TAAC G CT A TAGTTTTTGTCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTTGTCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A TAGTTTTTGTCT TA TTCT TAG ATCAAAAACGA GT AAGA ATC G AC C G CT A AGATGGGTG AGTGGT TCTACCTAC TCACCA A T CAA AAGATGGG GG GTGGT TTCTACTT CC CACCA TC CA T AGATGGGTGG AG GGT TCTACCCACC TC CCA CCG
GAM21	LOC145622	3'	CTATAGAACAAATGCAAAAAC	322	
GAM21	LOC222681	3'	CTACAGAACATGGAGCAAAAAC TA	386	
GAM21	LOC257507	3'	CTACAGAACATGGAGCAAAAAC TA	405	
GAM21	LOC257625	3'	CTACAGAACATGGAGCAAAAAC TA	406	
GAM22	BTEB1	3'	ACCACTACATCCATCT	53	
GAM22	CEP2	3'	ACCACCTCCTTCATCTT	112	
GAM22	ECM1	3'	ACCCTGCCCCACCCATCT	82	
GAM22	ENG	3'	ACCACITGGCCACGCTGTT	34	
GAM22	ESRRG	3'	ACCACITTTTCAGCCATTT	276	G C AGATGG TGG AAGTGGT

GAM22	HDAC4	3'	ACCACTCGACTCATCTTG	98	TTTACC ACT TTCACCA G T GGCA TAAGATGGGT AGTGGT GTTCTACTCA TCACCA
GAM22	IL6	3'	ACCACTTGAACAATTTTA	41	GC GGTGG TAAGATG CAAGTGGT ATTTTAC GTTCACCA
GAM22	LRAT	3'	ACCACTTAAAAATATCTTA	259	AAA GTGGC TAAGATGG AAGTGGT ATTCTATT TTCACCA
GAM22	MYLK2	3'	ACCACTCGGGGCCCCCATCTTG	226	AAAA T A TAAGATGGG GGC AGTGGT GTTCTACCC CCG TCACCA
GAM22	PRKACB	3'	ACCACTTCTTTTCATCT	61	GGGC T C AGATGGG GG AAGTGGT TCTACTT TC TTCACCA
GAM22	PRLR	3'	ACCACTTGGCCTCTTTCT	51	T T AGA GGG GGCAAGTGGT TCT TCT CCGTTTCACCA
GAM22	SLC6A6	3'	ACCACTTGAATTGATCTT	65	T G GG AAGAT GGT CAAGTGGT TTCTA TTA GTTCACCA
GAM22	WASF3	3'	ACCACTTGGTCAGAAATTTTA	109	G A GGG TAAGAT TGGC AAGTGGT ATTTTA ACTG TTCACCA
GAM22	XK	3'	ACCACTTGCATATCTTA	181	AG G TG G TAAGA GGTG CAAGTGGT ATTCT TCAC GTTCACCA
GAM22	ZYX	3'	ACCACTTGGCCCCACCT	69	TA A T A AG TGGG GGCA GTGGT

GAM22	ARHF	3'	ACCTGGACCA	167	TC ACCC CCGT CACCA C - CA_ T AGATGGGTGG AG GGT TCTACCCACC TC CCA
GAM22	DDR1	5'	CGCACCA	57	AGG - CAA - TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	DDR1	5'	CGCACCA	122	A - CAA - TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	DDR1	5'	CGCACCA	123	A - CAA - TAAGATGGGTGG GTG ATTTTACCCACC CGC
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	141	A - TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA
GAM22	DKFZP547E1010	5'	ACCACCTCCCTATCTTA	280	CT - TG CAA TAAGATGGG G GTGGT ATTCTATCC C CACCA
GAM22	FLJ11715	3'	ACCGGCGCCAGCCCATCT	197	CT - AA AGATGGGT - GGC GTGGT TCTACCCG CCG CGCCA
GAM22	FLJ12587	3'	ACCAGGGCGCATCCATCT	190	AC - AAG AGATGG - GTGGC TGGT TCTACC CGCCG ACCA
GAM22	FLJ12650	3'	ACCACCTTGCCAAATGCCCTCTC	196	T - GG - GA GGGT - GGCAAGTGGT CT TCCG CCGTTCACCA
GAM22	FLJ13265	3'	ACCACCTTGCCCTGCCCTCA	201	C - TAA TG - GGT - GGCAAGTGGT

GAM22	FLJ20546	3'	ACCTCTGCCACCCATCT	155	<p>AC CCG CCGTTCACCA</p> <p>T TC</p> <p>A T</p> <p>AGATGGGTGGCA G GGT</p> <p> </p> <p>TCTACCCACCGT C CCA</p>
GAM22	FLJ32865	3'	ACCACCACGCCCAGCTTA	251	<p>A GCAA</p> <p>TAAAG TGGGTG GTGGT</p> <p> </p> <p>ATTC ACCCGC CACCA</p>
GAM22	GPR88	3'	ACCACTTGTTGTACATCT	185	<p>G TG</p> <p>AGATG G GCAAGTGGT</p> <p> </p> <p>TCTAC T TGTTACCA</p>
GAM22	HSPC216	3'	ACCTGACCACCCATT	149	<p>A GT</p> <p>AGATGGGTGG CA GGT</p> <p> </p> <p>TTTACCCACC GT CCA</p>
GAM22	JIK	3'	ACCACATTCCCCATT	148	<p>A T CAA</p> <p>TAAAGATGGG GG GTGGT</p> <p> </p> <p>ATTTTACCC CT CACCA</p>
GAM22	KIAA0153	3'	ACCACCAGCAAGCCCGCTTA	139	<p>A G AA</p> <p>TAAG TGGGT GC GTGGT</p> <p> </p> <p>ATTC GCCCG CG CACCA</p>
GAM22	KIAA0215	3'	ACCAGGAGACCACCATCTTA	130	<p>C AA ACC</p> <p>TAAGATGG TGG TGGT</p> <p> </p> <p>ATTCTACC ACC ACCA</p>
GAM22	KIAA0461	3'	ACCACTTGTTGAAATCCA	291	<p>AGAGG</p> <p>TGGGT GGCAAGTGGT</p> <p> </p> <p>ACCTA TTGTTACCA</p>
GAM22	MEGF10	3'	ACCACAGACTCATCTTA	216	<p>AAG</p> <p>TAAGATGGGT GTGGT</p> <p> </p> <p>ATTCTACTCA CACCA</p>
GAM22	MGC2452	5'	ACCACTTAATTGCCACTCA	218	<p>GA</p> <p>TGGGTGGCA AGTGGT</p> <p> </p>

GAM22	MGC4796	3'	ACCTTCACCTCATCTTTA	266	ACTCACCGT TCACCA TAA CAAGT TAAAGATG_GGTGG GGT ATTCTAC CCACT CCA T T T G AGATGGGTG CAA GTGGT TTTACCCAT GTT CACCA
GAM22	MRPL10	3'	ACCACATTGTACCCATTT	256	GG_G TAAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA
GAM22	MRPL42	5'	ACCACTTGATAAGCATCTTG	299	GG_G TAAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA
GAM22	POLYDOM	3'	ACCACTGCTATCCATCTT	195	GG_G TAAAGATG TG CAAGTGGT GTTCTAC AT GTTCACCA GA A AAGATGGGTGGCA GTGGT TTCTACCTATCGT CACCA
GAM22	PRO0246	5'	ACCACTTGCTATGGTCT	126	GG AGAT GTGGCAAGTGGT TCTG TATCGTTCACCA G_
GAM22	SMCR7	3'	ATGACTTGCCACCCACCT	247	A G AG TGGGTGGCAAGT GT TC ACCCACC GTTCA TA C G ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	TPD52	3'	ACCACCTTATATCAACTTA	88	ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	ZNF384	3'	ACCACCTCATCAGGCCATCTT	239	ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	LOC124216	3'	ACCTCTCCTCACCCTCTTA	307	ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT
GAM22	LOC144509	5'	ACCACCAAGCTGACCCATCT	320	ATG GC TAAG GGTG AAGTGGT ATTC CTAT TTCACCA AA_ A_ CA AAGATGG GTGG AGTGGT TTCTACC CACT TCACCA GG AC CA T TAAGATGGGTGG AG GGT ATTCTACCCACT TC GCA CC T AA AGATGGGTG GC GTGGT

GAM22	LOC146822	3'	ACCACCTGCCCTTACCATTT	324	TCTACCCAC CG CACCA GT AC GT A AGATGG GGCA GTGGT TTTACC CCGT CACCA ATC C G C AGATGG TGG AAGTGGT TCTACC GTC TTCACCA G A - AA A GATGGGTGGC GT GGT A TTACCCACCG CG CCA C GC T TAAGATGGG TGG GGT ATTCTACCC ACC CCA G CC G CAA TAAGATGG TGG GTGGT ATTTTACT ACC CACCA G TAAGATG GGTG AAGTGGT ATTCTAC CCGT TTCACCA T AATA G A AGATGG TGGCA GTGGT TCTACC GTCGT CACCA G TGGG TGGCAAGTGGT ATCC GCCGTTACCA TCGA G AAG TAAGATGGGT GC TGGT ATTCTATCCA TG ACCA A G CA AGATGG TGG AGTGGT
GAM22	LOC148371	5'	ACCATTCTGGCCATCT	330	
GAM22	LOC149373	3'	ACCTGCCGGCCACCCATTCA	333	
GAM22	LOC151146	5'	ACCCCCAGCCCATCTTA	336	
GAM22	LOC157562	5'	ACCACCAGTCATTTTA	357	
GAM22	LOC160897	3'	ACCATTATAATGCCCTCATCTT	341	
GAM22	LOC161589	5'	ACCACCTGCTGGCCATCT	343	
GAM22	LOC163682	5'	ACCATTGCGGAGCTCCTA	361	
GAM22	LOC199692	3'	ACCAGTAACCTATCTTA	257	
GAM22	LOC202108	5'	ACCACCTACTGGCCATCT	367	

GAM22	LOC221468	3'	ACCACCCAGTTTCTTCATCTT	258	<p>TCTACC GTC TCACCA</p> <p>G A_ TG AA_</p> <p>AAGATGG GC GTGGT</p> <p> </p> <p>TTCTACTT TG CACCA</p> <p>CT ACC</p>
GAM22	LOC221838	5'	ACCACTACTGGCCATCT	385	<p>G CA</p> <p>AGATGG TGG AGTGGT</p> <p> </p> <p>TCTACC GTC TCACCA</p>
GAM22	LOC221839	5'	ACCACTACTGGCCATCT	384	<p>G A_</p> <p>G CA</p> <p>AGATGG TGG AGTGGT</p> <p> </p> <p>TCTACC GTC TCACCA</p>
GAM22	LOC90313	5'	ACCACCCCTGTGCCCATC	268	<p>G A_</p> <p>G A_</p> <p>GATGGTG CA GTGGT</p> <p> </p> <p>CTACCCGT GT CACCA</p> <p>CCC</p>
GAM22	LOC92399	3'	ACCACCTGTCTCTCATCTTA	242	<p>TG A</p> <p>TAAGATGGG GCA GTGGT</p> <p> </p> <p>ATTCTACTC CGT CACCA</p> <p>CT C</p>
GAM23	ADAM8	3'	AGAGAAGCCATGCGTTCC	52	<p>A T CAA</p> <p>C GAC CAT GCTTCTCT</p> <p> </p> <p>C TTG GTA CGAAGAGA</p> <p>C C C_ AA T</p>
GAM23	BN51T	3'	AGAGAGCAAGGATTGAGTCTG	363	<p>CAGACTCA TC GCT CTCT</p> <p> </p> <p>GTCTGAGT AG CGA GAGA</p> <p>T GAA</p>
GAM23	CD3Z	3'	AGACTGACCTTGATGAGCTG	48	<p>A C C_</p> <p>CAG CTCATCAAG TT TCT</p> <p> </p> <p>GTC GAGTAGTTC AG AGA</p>
GAM23	DAAM2	3'	AGGTGCTTGATGAATCTG	381	<p>C T</p> <p>CAGA TCATCAAGC TCT</p> <p> </p> <p>GTCT AGTAGTTCG GGA</p> <p>A T</p>
GAM23	DLG4	3'	AGGAGGGATGGGTCT	54	<p>AAG</p> <p>AGACTCATC CTTCTCT</p> <p> </p>

GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	73	<p>TCTGGGTAG GGAGGGA</p> <p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	74	<p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	DMD	5'	AGAAAAGCTTGAGCAAGTC	75	<p>CA_ C</p> <p>GACT TCAAGCTT TCT</p> <p> </p> <p>CTGA AGTTCGAA AGA</p> <p>ACG A</p>
GAM23	E2F1	3'	AGGCCCTCTTTGGTGAGCCCTG	348	<p>A</p> <p>CAG CTCATCAA GCTT</p> <p> </p> <p>GTC GAGTGGTT CGGA</p> <p>C TCTC</p>
GAM23	EBP	3'	AGAGAAAGCCAGGAGGTCT	108	<p>CA AA</p> <p>AGACT TC GCTTCTCT</p> <p> </p> <p>TCTGG AG CGAAGAGA</p> <p>GAC</p>
GAM23	FANCG	5'	AGAGAAAGCAGGGGAGCTC	85	<p>A AA</p> <p>GA CTC TC GCTTCTCT</p> <p> </p> <p>CT GAG GG CGAAGAGA</p> <p>C GA</p>
GAM23	FE65L2	5'	AGGGCCCTGATGAGTTCA	99	<p>A A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGGCCCTGATGAGTTCA	236	<p>A A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGGCCCTGATGAGTTCA	237	<p>A A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>
GAM23	FE65L2	5'	AGGGCCCTGATGAGTTCA	238	<p>A A T</p> <p>C GACTCATCA GC TCT</p> <p> </p> <p>A TTGAGTAGT CG GGA</p> <p>C C C</p>

Gene	Accession	Position	Sequence	Length
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	193
GAM23	FGFR4	3'	AGAGAAGCTGGAAGCCTG	58
GAM23	FHL1	3'	AGAGAAGCTGATGCCTC	55
GAM23	GCNT2	5'	AGAGAAACGAGTGAGTTTG	56
GAM23	GNRHR	5'	AGAGAAGCTGGTAATTCTG	38
GAM23	HIS1	5'	AGGGGAGATGAGTTTG	105
GAM23	HNRPDL	3'	AGAAAGGTATGAGTTTG	92
GAM23	INHBA	3'	AGAAAGCCATGAGTTTG	59
GAM23	KIF3B	3'	AGAGAAGCTCATAAGTG TG	87
GAM23	MSN	3'	AGAGAAGCCTGTGCCCTG	262

GAM23	MTR	3'	AGAGAAGTGTGACCCCTG	36	GTC GT GT CGAAGAGA CC_ C AC _CAA CAG TCAAT GCTTCTCT GTC AGTG TGAAGAGA
GAM23	PCDHB9	3'	AGAGAAGTTAGATCCTG	169	CC_ A ACTC _ CAG ATC AGCTTCTCT GTC TAG TTGAAGAGA
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG	246	C_ A TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA
GAM23	SMARCA3	3'	AGAGAAGCTTCATGTTTG	66	TAC TCATC CAGAC AAGCTTCTCT GTTTG TTCGAAGAGA
GAM23	SMG1	3'	AGACAGTAGATGAGTCTG	138	TAC_ AA CAGACTCATC GCT_TCT GTCTGAGTAG TGA AGA
GAM23	SNCAIP	5'	AGAAAGGGGTGAGTCTG	399	A_ C AAG C CAGACTCATC CTT TCT GTCTGAGTGG GAA AGA
GAM23	SYNGR1	3'	AGGGGAGCGATGAGCTG	86	GG_ - A AA_- CAG CTCATC GCTTCTCT GTC GAGTAG CGAGGGGA
GAM23	UCP2	5'	AGAGAAGCTTGATCTTGGAG	68	_- CTC_ ATCAAGCTTCTCT GAG TAGTTCGAAGAGA
GAM23	BMF	3'	AGAGGCTGATGTGTCTG	229	GTTC T A CAGAC CATCA GCITCT GTCTG GTAGT CGGAGA
GAM23	BNIP2	3'	AGAGAATGTGATGAGTT	278	T AG_ GACTCATCA TTCTCT

GAM23	DDX33	3'	AGAGAAAGCCTTGAATC	171	TTGAGTAGT AAGAGA GT _ C AT GA TC CAAG _CTTCTCT CT AG GTTC GAAGAGA A _ C GACTCATC _AAG TTCT TTGAGTAG TTC AAGA GT A CAAG AGACTCAT CTTCCTCT TCTGGGTA GAAGAGA AA A CA AA CAG CT TC GCTTCTCT GTC GG AG CGAAGAGA C CA A_ A T T A AG C CA CA GCTTCTCT TC G GT GT CGAAGAGA C _ _ G T A _ _ G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA G _ T A _ G T CAG CTCATCAA C TCT GTC GAGTAGTT G AGA G _ T C _ TCAA CAGA TCA GCTTCTCT GTCT GGT CGAAGAGA AC TGA CA A GACT TC AGCTTCTCT CTGA AG TCGAAGAGA A AC CA CAG TCAT AGCTTCTCT
GAM23	EML4	3'	AGAAACTTTGGATGAGTT	168	
GAM23	EPB41L4	3'	AGAGAAAGAAATGGGTCT	187	
GAM23	FLJ11588	5'	AGAGAAAGCAGAACGGCCTG	199	
GAM23	FLJ20150	3'	AGAGAAAGCCTGTGGCT	153	
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG	154	
GAM23	FLJ20507	3'	AGATGTTGATGAGGCTG	261	
GAM23	FLJ20972	3'	AGAGAAAGCAGTTGGCATCTG	205	
GAM23	FLJ22233	3'	AGAGAAAGCTAGAAGTC	204	
GAM23	FLJ23191	3'	AGAGAAAGTTGTGACCTG	198	

GAM23	FLJ23468	5'	AGAGAAACCAAGTCAGTCTG	200	<p>GTC AGTG TTGAAGAGA</p> <p>C_ TCAA TCTCT</p> <p>CAGACTCA GCT TCTCT</p> <p> </p> <p>GTCTGAGT CGA AGAGA</p> <p>CCAA</p>
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	133	<p>C CAA</p> <p>AGACT AT GCTTCTCT</p> <p> </p> <p>TCTGA TA CGAAGAGA</p>
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	231	<p>C CAA</p> <p>AGACT AT GCTTCTCT</p> <p> </p> <p>TCTGA TA CGAAGAGA</p>
GAM23	GIT2	3'	AGAGAAGCATCAGTCT	232	<p>C CAA</p> <p>AGACT AT GCTTCTCT</p> <p> </p> <p>TCTGA TA CGAAGAGA</p>
GAM23	GRID1	3'	AGAGAAGCCTAGGTGGCT	285	<p>A AA_</p> <p>AG CTCATC GCTTCTCT</p> <p> </p> <p>TC GGGTGG CGAAGAGA</p> <p>ATC</p>
GAM23	GT650	3'	AAGCTTTCATGAGTTTG	230	<p>C_</p> <p>CAGACTCAT AAGCTT</p> <p> </p> <p>GTTTGAGTA TTCGAA</p> <p>TCT</p>
GAM23	IKKE	3'	AGGACTGTGAGTCTG	124	<p>CA C</p> <p>CAGACTCAT AG TTCT</p> <p> </p> <p>GTCTGAGTG TC AGGA</p>
GAM23	KIAA0254	5'	AGAGGACCGGATGATC	131	<p>AA_</p> <p>GACTCATC GC TTCTCT</p> <p> </p> <p>CTGAGTAG CG AGAGA</p> <p>CC</p>
GAM23	KIAA1026	3'	AGAGAAGCTGCCTCAGTCTG	292	<p>CATCA</p> <p>CAGACT AGCTTCTCT</p> <p> </p> <p>GTCTGA TCGAAGAGA</p> <p>CTCCG</p>
GAM23	KIAA1163	3'	AGAGAAGCATGTCTGAGTT	331	<p>T_ A</p> <p>GACTCA CA GCTTCTCT</p> <p> </p>

GAM23	KIAA1598	3'	AGAAAGCTTCTGTTTTTGGGTCTG	161	TTGAGT GT CGAAGAGA CT A TC CAGACTCA AAGCTTCT GTC TGGGT TTCGAAGA TTTGTC CAA CAGACTCAT GCTTCT GTC TGGGT CGAAGA A CT A GA CATCA GCTTCTCT CT GTGGT CGAAGAGA AG CA A CAGACT TCA GCTTCTCT GTTTGA AGT CGAAGAGA G TCA GACT CA AGCTTCTCT TTGA GT TCGAAGAGA A TTC A A CAG CTC TCAA GCTTCT GTC GAG AGT CGAAGA C T CAGACTCAT AGCTTCT GTC TGGGT TCGGAGA
GAM23	KIAA1853	3'	AGAAGCAATGGGTCTG	287	C CA GA TC AT AGCTTCTCT CT AG TG TCGAAGAGA A A AC A A AA CAG CTC TC GCTTCTCT GTC GAG AG TGAAGAGA C A GA ATCAA CAGACTC GCTTCTCT
GAM23	LOXL4	3'	AGAGAAGCTGGTGGATC	213	
GAM23	METAP1	3'	AGAGAAAGCGTGAAGTTTG	298	
GAM23	MGC11034	3'	AGAGAAAGCTCTTTTGAAGTT	211	
GAM23	MGC14128	3'	AGAAGCTTTGAGAGCCTG	222	
GAM23	MGC16175	5'	AGAGGCTGTGAGTCTG	219	
GAM23	MGC2752	5'	AGAGAAAGCTCAGTAGAATC	327	
GAM23	MGC34923	3'	AGAGAAAGTAGGAAGAGCCTG	254	
GAM23	NR113	5'	AGAGAAAGCAGGAGTCTG	89	

Accession	Gene	Position	Sequence	Length
GAM23	NYD-SP15	3'	AGAGAAGAAATATTTGAGTCTG	208
			GTCTGAG CAAAGAGA GA TCAAG CTTCTCT CAGACTCA GTCTGAGT GAAGAGA TTATAAA ATCAA CAGACTC GCTTCTCT GTCTGGG TGAAGAGA GT CA CT CAGACTCAT AG TCTCT GTCTGAGTG TC AGAGA CC CAGACTCA TCA TCTCT GTCTGAGT AGT AGAGA T TCAA T CAGACTCA GCT CTCT GTCTGAGT CGA GGA T CT TCA CAGA CA AGCTTCTCT GTCT GT TCGAAGAGA AT TTC A AA CAG CTCATC GCTTCTCT GTC GAGTAG TGAGGAGA C G TCAA C CAGACTCA GCTT TCT GTCTGGGT CGAA AGA TTTGGG A CT T CAGA CA CAAGCTTCTCT GTTT GT GTTCGAAGAGA TT GC CAGACTCAT CAA TTCTCT 	
GAM23	OSBPL8	5'	AGAGAAGTTGGGTCG	177
GAM23	PLEKHA4	5'	AGAGACCCCTGTGAGTCTG	178
GAM23	PRKWNK2	3'	AGAGATGATTGAGTCTG	372
GAM23	PSMD4	3'	AGGGTAGCTGAGTCTG	63
GAM23	RIS1	3'	AGAGAAGCTCTTTGTATCTG	337
GAM23	RNF24	3'	AGAGGAGTGGATGAGCCTG	114
GAM23	SNURF	3'	AGAAAAGCGGTTTGGGTCG	96
GAM23	SULT4A1	3'	AGAGAAGCTTGTGTTTTTG	284
GAM23	SV2B	3'	AGAGAATTGTGTGAGTCTG	135

GAM23	SZF1	5'	AGAGAAAGCCTAGATATCTG	147	GTCTGAGTG GTT AAGAGA T CTC AA CAGA ATC GCTTCTCT GTCT TAG CGAAGAGA A ATC TCAAG CAGACTCA CTTCTCT GTCTGAGT GGAGAGA TATG C T GA TCA CAAGCTTCTCT CT AGT GTTCGAGGAGA A AAG CAGACTCATC CTTCT GTTTGAGTAG GAAGA
GAM23	TLR10	5'	AGAGAGGGTATTGAGTCTG	210	
GAM23	ZNF185	3'	AGAGGAGCTTTGTGAATC	111	
GAM23	LOC113612	3'	AGAAAGGATGAGTTTG	300	
GAM23	LOC133539	3'	AGAGAAAGCCAGGATGGTC	312	T AA GAC CATC GCTTCTCT CTG GTAG CGAAGAGA GACC AC CAA CAG TCAT GCTTCTCT GTC AGTA CGAAGAGA C CA CAGACTCAT CAA GCTT GTCTGAGTA GTT TGAA AT ATT AA T CAGACTCATC GCT CTCT GTCTGAGTGG TGA GAGA GGG A ATCA CAG CTC AGCTTCTCT GTC GAG TCGAAGAGA AACGG CA C GACT TCAAGCTT TCT
GAM23	LOC139221	5'	AGAGAAAGCACATGACCTG	313	
GAM23	LOC142941	3'	AAGTTTATTGTAATGAGTCTG	345	
GAM23	LOC145717	5'	AGAGAGTGGGGTGAGTCTG	279	
GAM23	LOC147229	3'	AGAGAAAGCTGGCAAGAGCTG	325	
GAM23	LOC147658	3'	AGAAAAAGTTTGAAGTC	326	

[illegible]

GAM23	LOC200020 3'	AGAAAGCGGTGAGTC	371	CTGAGTGG CGGA AGA A AA C GACTCATC GCTT TCT CTGAGTGG CGGA AGA
GAM23	LOC200226 3'	AGAGAAAGCTCGTGAATGTT	365	A CA GAC TCAT AGCTTCTCT TTG AGTG TCGAAGAGA
GAM23	LOC204820 5'	AGAGAAAGCCAGGCCAGCTG	373	TA C A CA AA CAG CT TC GCTTCTCT GTC GA GG CGAAGAGA
GAM23	LOC219392 5'	AGAGAAAATCCTAGATGAGTC	377	- CC AC A C GACTCATC AG TTCTCT CTGAGTAG TC AAGAGA
GAM23	LOC219800 3'	AGAGAAAGCTTGGGAGCCT	389	A A A A AG CTC TCAAGCTTCTCT TC GAG GGTTCTGAAGAGA
GAM23	LOC220753 5'	AGAGAAAGCCAGAGGTGTG	388	C G CA AA CA ACT TC GCTTCTCT GT TGG AG CGAAGAGA
GAM23	LOC220776 3'	AGAGGGGTGATGATAAACTG	283	G AC AC AA CAG TCATC GCTTCTCT GTC AGTAG TGGGGAGA
GAM23	LOC221454 5'	AGAGAAAGATGAAGTTTG	382	AAAT CA AG CAGACT TCA CTTCTCT GTTTGA AGT GAAGAGA
GAM23	LOC222444 3'	AGAGAAAGCCAGGATGCTC	392	A A T AA GAC CATC GCTTCTCT CTG GTAG CGAAGAGA
GAM23	LOC222962 3'	AGAGGGGAGGTAAGTCTG	387	- C AAG GACC CAGACT ATC CTTCTCT

GAM23	LOC245727	5'	AGAGAGTGGGGTGAGTCTG	376	GTCTGA TGG GGGGAGA A A_ AA_ T CAGACTCATC GCT CTCT GTCTGAGTGG TGA GAGA GGG CATCA CAGACT AGCTTCTCT GTTTGG TCGAAGAGA ACG CTCAT CAGA CAAGCTTCTCT GTTT GTTTGAAGAGA AAAT ATCAA CAGA CTC GCTTCTCT GTCT GAG CGAAGAGA C C A A C AG CTCATCAAG TTCT TC GAGTAGTTC AAGA A CAGACTCATC CTCTCT GTTTGAGTAG GAAGA A_ C_ A III C GA AC CAG TTGTA T AC CT TG GTC AACAT A TATAC TA C III C C_ A III TG GA AC CAG TTGTA T AC CT TG GTC AACAT A TATAC TA C III A A C TCC AA TG GAACCCAG AGG TT AC CTTGGGTT C C G C TGC AA CCAGATTGTA
GAM23	LOC253525	5'	AGAGAAAGCTGCAGGTTTG	401	
GAM23	LOC254249	5'	AGAGAAAGTTTGTAATTTG	397	
GAM23	LOC255475	5'	AGAGAAAGCCGAGCTCTG	403	
GAM23	LOC51026	3'	AGAAACCCTTGATGAGACT	146	
GAM23	LOC91308	5'	AGAAAGATGAGTTTG	274	
GAM24	CASP10	3'	ATACAACTGATGTCATATTCC ATTTTGGG	223	
GAM24	CASP10	3'	ATACAACTGATGTCATATTCC ATTTTGGG	224	
GAM24	CHRN3	5'	TTGGGTTCCACTTCGGA	49	
GAM24	LANCL1	3'	TACAATCTGGACTTTGGTA	100	

GAM24	MS4A3	3'	ACATCTGGGTTCAAATTCTG	101	ATG TT GGTCTAACAT G CA A GC T CA AAT GAAACCCAGAT GT GT TTA CTGGGTCTA CA C AA CCA ATGCGAAC GATTGTA TACGCTTG TTAACAT ACCTG A C_ AGA TCCA AATGCGAA CC TTGTA GGGT TTACGCTT GG AACAT C TA
GAM24	SLC1A4	3'	TACAAATTGTCCAGTTCCGAT	64	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGTTTAC CT GGGTT C GA AA GAAC TCCA TGC CCAGATTG AGGT ACG GGTCTGAC CC ACCA A C TCCA AATG GAA CCCAG AGGT TTAC CTGGGTT C A TCCA AATGCG ACCAG AGGTTTACGT TGGGT C TCCA AATG GAA CCCAG ATTGT
GAM24	ALLC	5'	TACAAGGATTTCGCATTCGGG	162	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATGCG ACCAG AGGTTTACGT TGGGT C TCCA AATG GAA CCCAG ATTGT
GAM24	APOL6	3'	CTGGGTTACATTTTGGG	206	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	CBX6	3'	TTGGGCTCCATTCCTGGA	128	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	FLJ10055	3'	TTGGGAGTCCCATTTTGGG	156	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	FLJ22059	5'	CAGTCTGGACCGACCTTGGG	191	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	KCNH8	3'	TTGGGTTCCATTCCTGGA	252	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	KIAA0870	3'	TTGGGCTCTGCATTTTGGG	339	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT
GAM24	KIAA1157	3'	ACAGTATTCATTTTGGG	296	TCCA AATG GAA CCCAG AGGTTTAC CTGGGTC A A C A TCCA AATG GA CCCAG AGGT TTAC CT GGGTT C C C A_ CCCAG AGGT TTAC CTGGGTT C A TCCA AATG GAA CCCAG ATTGT

GAM24	PRO1048	3'	ACAAATGAGTTTGCAATTTT	163	AGGTTTTTAC CTT TGACA - C GA AAAAATGCGAAC CA TTGT TTTTACGTTTG GT AACA
GAM24	PRO1787	3'	ACAAATTCGCAATTTTG	165	A AACCCA CAAAATGCG GATTGT GTTTTACGC TTAAACA
GAM24	UBE2G1	3'	TACAGATGATTACGCATTTTG	67	C AACC GA CAAAATGCG CA TTGTA GTTTTACGC GT GACAT
GAM24	LOC122402	3'	TACTTCTTGGTTTCACATTTTGG	306	ATTA A C C TT TCCAAAATG GAACC AGA GTA AGGTTTTTAC CTGG TCT CAT
GAM24	LOC153592	3'	GGAAATTCAGCAATTTTGGGA	355	A T T C C TCCAAAATGC GAA CC AGGTTTTTACG CTT GG
GAM24	LOC256158	5'	ACAAATCTGAACGTCGTGGG	404	A AA AAAT AACC TCCA GCG CAGATTGT GGGT TGC GTCTAACA
GAM25	ITGA5	3'	CTCAGATCCAGGGACAGAGG	264	C AA GTTAGA A TCTCTG CC GATCTGAG GGAGAC GG CTAGACTC
GAM25	SF3B3	3'	GCTCTAGAATCTTAACCAGA	116	AG AC CCAGA TCTGGTTTGA TCT GAGC AGACCAATCT AGA CTGG
GAM25	SLC4A4	3'	GCTCAGAGTTGTTAACCAGA	71	A T AC A TCTGGTTTGA CAG TCTGAGC AGACCAATT GTT AGACTCG
GAM25	ZNF180	3'	CTCAGACCTGAATCAGAGA	120	G AGAC A TCTCTGGTT CAG TCTGAG

GAM25	AP1G2	5'	GCCCAGGCACGCCCGACCAGAG	233	AGAGACTAA	GTC	AGACTC
			A		AGACCAGA	A	
					TCTCTGGTT	TCTG	GC
					AGAGACCCAG	GGAC	CG
					CCCGCAC	C	
GAM25	BCL2L1	3'	GCCCAGATCTGGTCCCTTGCAG	241	GTTA	A	
					CTG	GACCAGATCTG	GC
					GAC	CTGGTCTAGAC	CG
					GTTCC	C	
GAM25	FLJ25012	5'	CTCAGATCTGAAAAAGCACAAGA	250	TCT	AGAC	
					TG	GTT	CAGATCTGAG
					AGA	AC	CGA
					GTCTAGACTC		
GAM25	FLJ31952	3'	CAAAATCTGGTTCTGAAAG	253	GG	AAA	C
					CT	TTAGA	CCAGAT
					GA	AGTCT	GGTCTA
					AC	A	
GAM25	MDS025	3'	CTCAGACCTGGTTTGAGATAGA	184	TCTG	TTAGACCAG	TCTGAG
					AGAT	AGTTGGTC	AGACTC
GAM25	MGC32043	3'	GCTCAGATCTGATGCTTCAAGA	249	AG	C	
					GGTT	AC	CAGATCTGAGC
					TCT	AG	
					AGA	TC	GTCTAGACTCG
GAM25	MSI2	3'	CTCCCCATCCCAACCAGAGA	245	ACT	GTA	
					CT	AGACCA	CT
					TCTCTGGTT	GAT	GAG
					AGAGACCAA	CTA	CTC
GAM25	ZNF271	5'	GCTCAGATCTGGTTAAACATCA	395	CC	CCC	
			GAGA		A		
					TCTCTG	GTT	GACCAGATCTGAGC
					AGAGAC	CAA	TTGGTCTAGACTCG
GAM25	LOC144508	5'	GCTCAGATCCATGTGCCAGGGA	362	TA	A	
					TAGACCA		
					TCTCTGGT	GATCTGAGC	
					AGGGACCG	CTAGACTCG	
					TGTAC		
GAM25	LOC145845	3'	CTCAAAATCCCAACCAGAGA	346	TAGACCA	C	
					TCTCTGGT	GAT	TGAG

GAM26	CDH19	3'	GAAAAATTTAAAGGAGCAA	182	AGAGACCA CTA ACTC CC A A_ CTTTAAATTTTC AACG GAAATTTTAAAG AG T CTTTAA_ TTTTCCCA TTGGT GCA AACCA CGT AAAAGGGT - C A TTGGTTG ACTTT AATTTTC AATCAAC TGAAA TTAAAAG A AG TTGGTTGCA TTT TTTTCC AACCAACGT AGA AAAAGG C AA CTTTAA TTGGTTGCA ATTTTC AACCAACGT TAGAAG AA GC TAAATTT TCCCA TTGGTT ACTT AACCAA TGAA AGGT A_ C TT GCACTTTAAATTTTC CA GATC TGTGAAATTTAAAG GT TT A GC TTAAA TTGGTT ACT TTTTCCC AACCAA TGA AAAAGGG A_ CG ATT G CACTTTAA TTCC AACCAA GTGAAATT GAGG G AT_ A AAA TTGGTTGC CTTT TTTTC
GAM26	CRYGS	5'	TGGGAAAACCACTCTATGCACC	152	AA
GAM26	CYP1B1	3'	GAAAAATTGAAAAAGTACAACCTAA	33	
GAM26	GLI3	3'	GGAAAAAAGACTGCAACCAA	35	
GAM26	PCLO	3'	GAAGATAATGCAACCAA	391	
GAM26	PPP2R5A	3'	TGGGAAAGTAAACCAA	102	
GAM26	PTER	3'	TGAGAAAATTTAAAGTGTTTCT	207	AG
GAM26	REF5	3'	GGGAAAAGCAGTAAACCAA	39	
GAM26	CSMD1	3'	GGAGTATTAAAGTGGAACCAA	301	
GAM26	MGC15438	3'	GAAAGAAAGCGCAGCCAA	220	

GAM26	NYD-SP18	3'	GGAGAAAACTGCAACCAA	217	AACCGACG GAAA GAAAG C C AAAT TTGGTTGCA TTT TTTCC AACCAACGT AAA AGAG C C TAAA TTGGTTGCA TT TTTTCC AACCAATGT AA AAAAGG TA CACTTTAA TTGGTTG ATTTTCCC AACCAAC TAGAAGGG ACG A TAA TTGGTTGC CTT ATTTT AACCAACG GAA TAAGA C CAGG G G ATTT TTGGTT CACTTTAA TCC AACCA GTGAAATT AGG G AC AAT TTGGTTGC TTTA TTTCC AACCAACG AAAT AAAGG GT ATT TAA TTGGTTGCACTT ATTTT AACCAACGTGAA TAAAG CGG C CCC C GG AACGA CT GTCACAAT CC TTGTT GA CAGTGTTA A AA A TGGCAAC GACCC CT GT ACCGTTG CTGGG GA CG T G CTGTC TGGCAAC ACCC ACAATA
GAM26	OLF3	3'	GGAAAAAATAATGTAACCAA	340	
GAM26	RPL13A	3'	GGGAAGATGCACAACCAA	115	
GAM26	LOC129452	3'	AGAAATGGACAAGCGCAACCAA	310	
GAM26	LOC150197	3'	GGATTAAAGTGAACCAA	335	
GAM26	LOC162239	3'	GGAAATTATAAATGGCAACCAA	344	
GAM26	LOC219972	3'	GAAATGGCAAGTGCAACCAA	379	
GAM27	DDX6	3'	ATTGTGACAAGAATTGTTACC	80	
GAM27	LOC126917	3'	GCAGTGGTCTGTTGCCA	309	
GAM27	LOC170395	3'	TATTGTTTCTGGGTGTTGCCA	316	

GAM28	ABCC3	3'	TGCCCCCTGGCTGTGCTCTAC	170	<p>ACCGTTG TGGG TGTTAT</p> <p>C A_ T TC TT_</p> <p>GTG AG ACA CCAGGGGCA</p> <p> </p> <p>CAT TC TGT GGTCCCGT</p> <p>C G C</p> <p>AGAAC_ ATCCAGGGGCA</p> <p> </p> <p>TACG TAGGTCCCGT</p> <p>ACCATC</p> <p>AGAAC_ ATCCAGGGGCA</p> <p> </p> <p>TACG TAGGTCCCGT</p> <p>ACCATC</p> <p>CA AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA_ AC</p> <p>TAGTG GA ATCCAGGG</p> <p> </p> <p>ATCAC CT TAGGTCCC</p> <p>A_ CC</p> <p>CA_ TCCAGGGGCA</p> <p> </p> <p>CAT TTTGT AGGTCCCGT</p> <p>CC AC</p> <p>G CA</p> <p>TAGT CAG AACATC GGGGCA</p> <p> </p> <p>GTCG GTC TTGTAG CCCCCT</p> <p>G C AC</p> <p>T C CA</p> <p>A AGTG AGAACATC GG</p> <p> </p> <p>A TCAC TCTGTGG CC</p> <p>C A A_</p> <p>TATAGTCAGA AT CCA</p> <p> </p> <p>ATATCACGTCT TA GGT</p> <p>CAT C</p> <p>CA</p> <p>AGTGCAGAA TCCA_ GGGGCA</p> <p> </p>
GAM28	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	225	
GAM28	CASP3	3'	TGCCCCCTGGATCTACCAGCAT	79	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	90	
GAM28	EMS1	3'	CCCTGGATCCTCACACTA	240	
GAM28	MLLT2	3'	TGCCCCCTGGACATGTTTCCTAC	97	
GAM28	TACCl	3'	TGCCCCCAGATGTTCTCTGGGCT	104	
GAM28	TNFSF6	3'	CCAGGTGTTCTACACTCA	42	
GAM28	UBB	3'	TGGCATTACTCTGCACTATA	166	
GAM28	AKAP10	3'	TGCCCCCTTTGGAATTCTGCACT	113	

GAM28	DECR2	3'	GCCCCCTCTGTCTCTGCAC	176	TCACGTCCTT AGGT CCCCCT A TT A TCC GTGCAGA ACA AGGGC CAGTCT TGT TCCCCG
GAM28	KIAA0240	3'	GCCCCCTGTGTCCCACTA	383	C C CA A TC TAGTG GA CA CAGGGC ATCAC CT GT GTCCCCG
GAM28	MGC16385	5'	GCCCCCTGGACGTTTCTGTCCGC	255	C A GTG CAGAA C TCCAGGGC CGC GTCCT G AGTCCCCG
GAM28	MGC5139	5'	GCCCCCTGGGCACACTGTA	305	C T C CAGAAC TATAGTG TCCAGGGC ATGTCAC GGGTCCCCG
GAM28	P5-1	3'	CCCCCTGGATGCCCTTAACCACT	110	AC C AA AGTG AG CATCCAGGG TCAC TC GTAGTCCCC
GAM28	TED	3'	CCCCCTGGGCCCTGCCCTA	143	CAA CCC T AACA TAG GCAG TCCAGGG ATC CGTC GGGTCCCC
GAM28	LOC133418	3'	TGCTCTAAAGCTCTGCACTA	311	CC ACATCCA TAGTGCAGA GGGCA ATCACGTCT TCTCGT
GAM28	LOC152402	3'	GCCCCCTTACATTCTGCACT	353	CGAA CATCC AGTGCAGAA AGGGC TCACGTCCT TCCCCG
GAM28	LOC158677	3'	TGCCCCCTGGATATACGAATAT	360	ACA G A AC TATA TGC GA ATCCAGGGCA ATAT ACG CT TAGGTCCCCG
GAM28	LOC221715	3'	CCACTGTGCTTGCACTA	390	A A A AA TC TAGTGCAG CA CAG GG

GAM28	LOC254746	3'	TGGCATTACTCTGCACTATA	394	ATCACGTT GT GTC CC C AC A TATAGTCAGA AT CCA ATATCACGTCT TA GGT CAT C TAGTGCAGA ACATCCA GGGGCA ATCACGTCT TCTCGT CGAA AG TATGG GCCTT GCATCTCC CAG CGAA CGTAGAGG GTC CT TA AGCCTTAGGC CT TGGCA TCGGAATCCG GA ACCGT C
GAM28	LOC255098	3'	TGCTCTAAAGCTCTGCACTA	396	AGC TTAGGCATC TCC TCG AATCCGTAG AGG A TGA GCCTTAGG TCCTC TGG CGGAGTCC AGAG ACC AC CTA GCCTTAGG TCCTC TGG CGGAGTCC AGAG ACC AC GCCTTAGG TC CCT GGCAG CGGAATCC AG GGA CCGTC AC CCC TTA CT G AGCC GGCATCTC AT GC TCGG CCGTAGAG TG TG CAC T G AGCCT AGGCAT ATGGCAG
GAM29	ADAM19	3'	CTGATGGAGATGCTCAAGGC	228	
GAM29	LFG	3'	TGCCACAGGCCCTAAGGCT	319	
GAM29	NOLA2	5'	GGAAGTGATGCCCTAAAGCT	393	
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC	158	
GAM29	FLJ10751	3'	CCAGAGACACCTGAGGC	159	
GAM29	FLJ10925	5'	CTGCCCCCAGGGACACCTAAGG	160	
GAM29	KIAA1118	3'	GTGGTTGAGATGCCACGGCT	289	
GAM29	KIAA1649	3'	CTGCCATTCTGTGCCTAGGCT	215	

GAM29	LIMR	3'	CTGCCATCTGCTGCTAGGC	157	TCGGG TCCGTG TACCGTC T ⁻ T ⁻ TCCTCT ⁻ GCCT AGGCA ATGGCAG CGGA TCCGT TACCGTC CGTC A CTA GCCTT GGCATCTC TGG CGGA CCGTAGAG ACC A AG ⁻ C C C ⁻ GC TTAGGCAT TC TATG CG AGTCCGTA AG GTAC A A AA AGCCT GGCAT TC TA GCAG TCGGA CCGTA AG GT TGTC C ⁻ A A GT CATCTC CTTAGG CTATGGCAG GAATCC GATACCGTC CATA ⁻ C A A GC TT GGCATCTCT TGGC CG AA CCGTAGAGGA ACCG A C C AGCCTT GC TATGGCA TCGGAA CG ATACCGT CT ⁻ A ⁻ A T ⁻ CTTAGGC TC CCTATGG GAATCCG AG GGATACC
GAM29	MGC14161	5'	CCAGAGAGATGCCAAAGGC	221	
GAM29	NJMU-R1	3'	CATGAAGAAATGCCCTGAAGC	188	
GAM29	SEMA3E	3'	CTGTTGTGAGAAATGCCCAAGC	119	
GAM29	YKT6	3'	CTGCCATAGATACCCCTAAG	106	
GAM29	LOC142972	5'	GCCACAGGAGATGCCCAAGC	271	
GAM29	LOC143689	3'	TGCCATAAGCTCAAGGCT	318	
GAM29	LOC148930	5'	CCATAGGGAGCCTAAG	332	
GAM29	LOC220469	3'	CCAAGGGATGCCCAAGC	317	
GAM29	LOC253782	3'	CATAAGAGCACCTAAGC	398	

CGGAATCC GAG ATAC
AC_ A CCTAT
AGCCTTAGGC TCT GGCA
|||||
TCGGAATCCG AGA CCGT
G C_

282

TGCCCAGAGGCCCTAAGGCT

5' LOC92078

GAM29